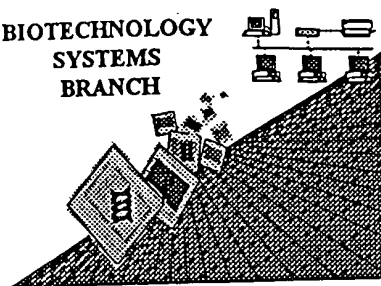S. Zhou

<u>RAW SEQUENCE LISTING</u>
<u>ERROR REPORT</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/422,838_

Art Unit / Team No. : _01PE_

Date Processed by STIC: _11/09/99_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/422,838_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION **US/09/422,838**

DATE: 11/09/1999
TIME: 11:02:24

Input Set: **I422838.RAW**

> This Raw Listing contains the General Information
> Section and up to first 5 pages.

[handwritten: these numeric identifiers and their responses are mandatory. please see item 13 on Exam summary sheet for a possible explanation of missing items]

Does Not Comply
Corrected Diskette Needed

E-->	1	<110> *[handwritten]*
E-->	2	<120>
W-->	3	<130>
	4	<140> US/09/422,838
	5	<141> 1999-10-22
E-->	6	<160> *[handwritten: see item 13 on Exam summary sheet]*
	7	<170> PatentIn Ver. 2.0
	8	<210> 1
	9	<211> 14
	10	<212> PRT
	11	<213> Artificial Sequence
	12	<220>
	13	<223> Description of Artificial Sequence: peptide
	14	<400> 1
	15	Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
	16	1 5 10
	17	<210> 2
	18	<211> 14
	19	<212> PRT
	20	<213> Artificial Sequence
	21	<220>
	22	<223> Description of Artificial Sequence: peptide
	23	<220>
	24	<223> Peptide is a subunit of a homodimer: Subunits in
	25	the dimer are covalently bonded at each carboxy
	26	terminus through peptide linkage with
	27	NH2-CH2-CH2-CH2-CH2-CH(CONH2)-NH-CO-CH2-CH2-NH2
	28	<400> 2
	29	Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
	30	1 5 10
	31	<210> 3
	32	<211> 684
	33	<212> DNA
	34	<213> Artificial Sequence
	35	<220>
	36	<223> Description of Artificial Sequence:
	37	oligonucleotide
	38	<400> 3
	39	atggacaaaa ctcacacatg tccaccttgt ccagctccgg aactcctggg gggaccgtca 60
	40	gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 120
	41	acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 180
	42	gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 240
	43	taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 300
	44	aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 360

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45        aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 420
46        aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 480
47        gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 540
48        tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 600
49        gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 660
                                                                             684
50        agcctctccc tgtctccggg taaa
51  <210> 4
52  <211> 684
53  <212> DNA
54  <213> Artificial Sequence
55  <220>
56  <223> Description of Artificial Sequence:
57        oligonucleotide
58  <400> 4
59        tacctgtttt gagtgtgtac aggtggaaca ggtcgaggcc ttgaggaccc ccctggcagt 60
60        cagaaggaga agggggggttt tgggttcctg tgggagtact agagggcctg gggactccag 120
61        tgtacgcacc accacctgca ctcggtgctt ctgggactcc agttcaagtt gaccatgcac 180
62        ctgccgcacc tccacgtatt acggttctgt ttcggcgccc tcctcgtcat gttgtcgtgc 240
63        atggcacacc agtcgcagga gtggcaggac gtggtcctga ccgacttacc gttcctcatg 300
64        ttcacgttcc agaggttgtt tcgggagggt cgggggtagc tcttttggta gaggtttcgg 360
65        tttcccgtcg gggctcttgg tgtccacatg tgggacgggg gtagggccct actcgactgg 420
66        ttcttggtcc agtcggactg gacggaccag tttccgaaga tagggtcgct gtagcggcac 480
67        ctcaccctct cgttacccgt cggcctcttg ttgatgttct ggtgcggagg gcacgacctg 540
68        aggctgccga ggaagaagga gatgtcgttc gagtggcacc tgttctcgtc caccgtcgtc 600
69        cccttgcaga agagtacgag gcactacgta ctccgagacg tgttggtgat gtgcgtcttc 660
                                                                             684
70        tcggagaggg acagaggccc attt
71  <210> 5
72  <211> 228
73  <212> PRT
74  <213> Artificial Sequence
75  <220>
76  <223> Description of Artificial Sequence: peptide
77  <400> 5
78        Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
79         1               5                  10                  15
80        Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
81                        20                  25                  30
82        Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
83                35                  40                  45
84        His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
85            50                  55                  60
86        Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
87        65                  70                  75                  80
88        Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
89                        85                  90                  95
90        Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
91                        100                 105                 110
92        Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
93                115                 120                 125
94        Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
```

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 95                   130                135                140
 96        Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 97        145                150                155                160
 98        Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 99                          165                  170                175
100        Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
101                          180                185                190
102        Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
103                 195                200             205
104        Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
105                 210                215                220
106        Ser Pro Gly Lys
107        225
108   <210> 6
109   <211> 8
110   <212> PRT
111   <213> Artificial Sequence
112   <220>
113   <223> Description of Artificial Sequence: peptide
114   <400> 6
115        Gly Gly Gly Lys Gly Gly Gly Gly
116            1               5
117   <210> 7
118   <211> 8
119   <212> PRT
120   <213> Artificial Sequence
121   <220>
122   <223> Description of Artificial Sequence: peptide
123   <400> 7
124        Gly Gly Gly Asn Gly Ser Gly Gly
125            1               5
126   <210> 8
127   <211> 8
128   <212> PRT
129   <213> Artificial Sequence
130   <220>
131   <223> Description of Artificial Sequence: peptide
132   <400> 8
133        Gly Gly Gly Cys Gly Gly Gly Gly
134            1               5
135   <210> 9
136   <211> 4
137   <212> PRT
138   <213> Artificial Sequence
139   <220>
140   <223> Description of Artificial Sequence: peptide
141   <400> 9
142        Gly Pro Asn Gly
143            1
144   <210> 10
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```
145    <211> 32
146    <212> PRT
147    <213> Artificial Sequence
148    <220>
149    <223> Description of Artificial Sequence: peptide
150    <400> 10
151         Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Pro
152          1               5                  10                  15
153         Asn Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
154                      20                  25                  30
155    <210> 11
156    <211> 36
157    <212> PRT
158    <213> Artificial Sequence
159    <220>
160    <223> Description of Artificial Sequence: peptide
161    <220>
162    <223> Cyclic peptide; Secondary structure is maintained
163         by disulfide bond between intramolecular Cys
164         residues at positions 9 and 31
165    <400> 11
166         Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly
167          1               5                  10                  15
168         Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu
169                      20                  25                  30
170         Ala Ala Arg Ala
171                      35
172    <210> 12
173    <211> 36
174    <212> PRT
175    <213> Artificial Sequence
176    <220>
177    <223> Description of Artificial Sequence: peptide
178    <400> 12
179         Ile Glu Gly Pro Thr Leu Arg Gln Cys Leu Ala Ala Arg Ala Gly Gly
180          1               5                  10                  15
181         Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Arg Leu Gln Cys Leu
182                      20                  25                  30
183         Ala Ala Arg Ala
184                      35
185    <210> 13
186    <211> 36
187    <212> PRT
188    <213> Artificial Sequence
189    <220>
190    <223> Description of Artificial Sequence: peptide
191    <400> 13
192         Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu Ala Ala Arg Ala Gly Gly
193          1               5                  10                  15
194         Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Ala Leu
```

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/422,838

DATE: 11/09/1

TIME: 11:02:2

Input Set: I422838.RAW

                                20   25   30
    195
    196   Ala Ala Arg Ala
    197   35

VERIFICATION SUMMARY
PATENT APPLICATION US/09/422,838

DATE: 11/09/19
TIME: 11:02:24

Input Set: **I422838.RAW**

Line	?	Error/Warning	Original Text
1	E	Response to "Applicant" Name is Missing	
2	E	Response to "Title of Invention" Missing	
3	W	Response to "File Reference" is Missing	
6	E	# of Seq. 0 Not Equal Actual 46	